

*Fig. 1*

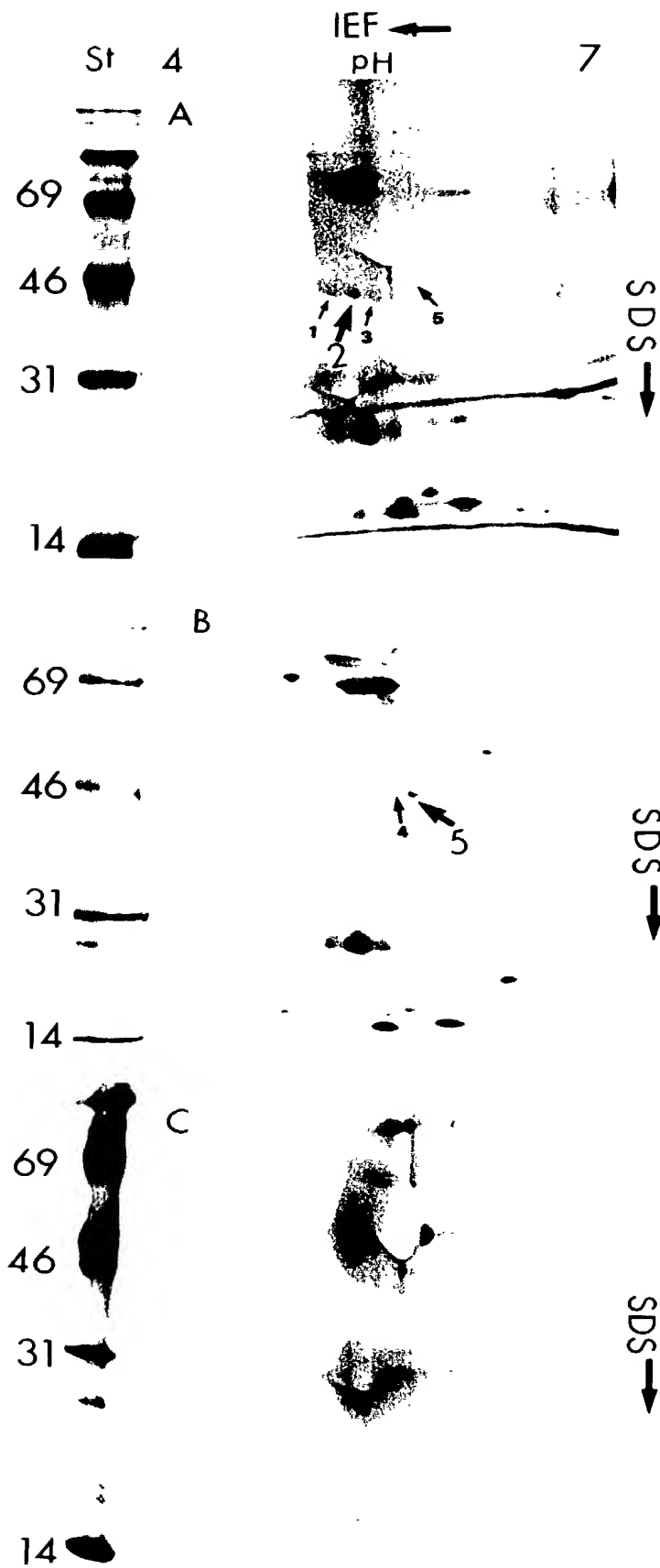
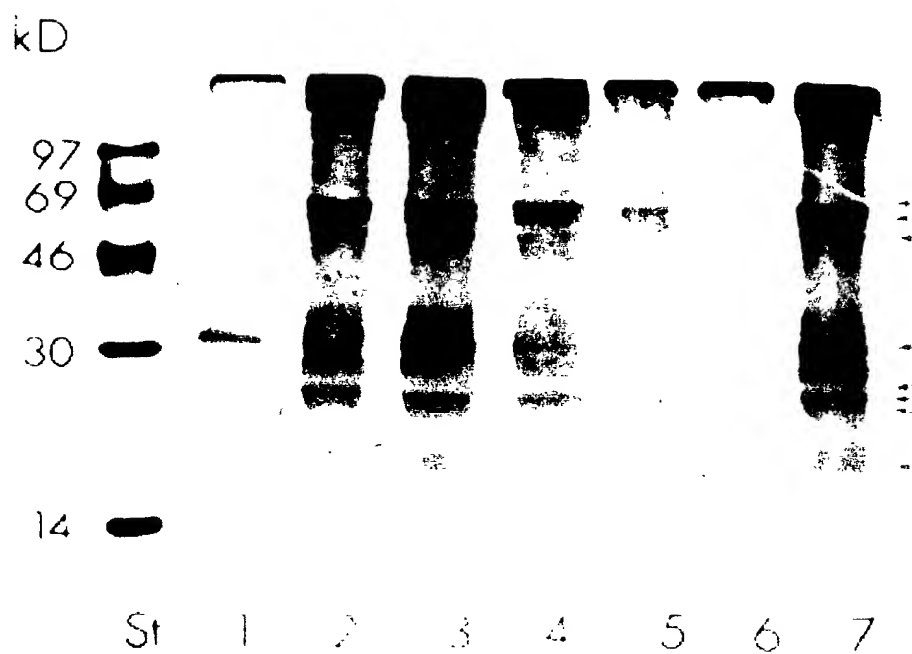
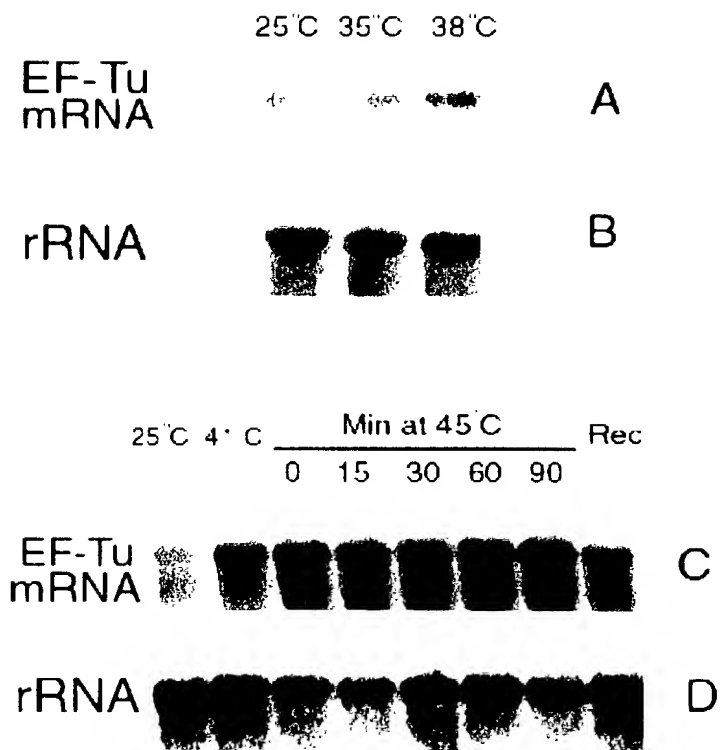


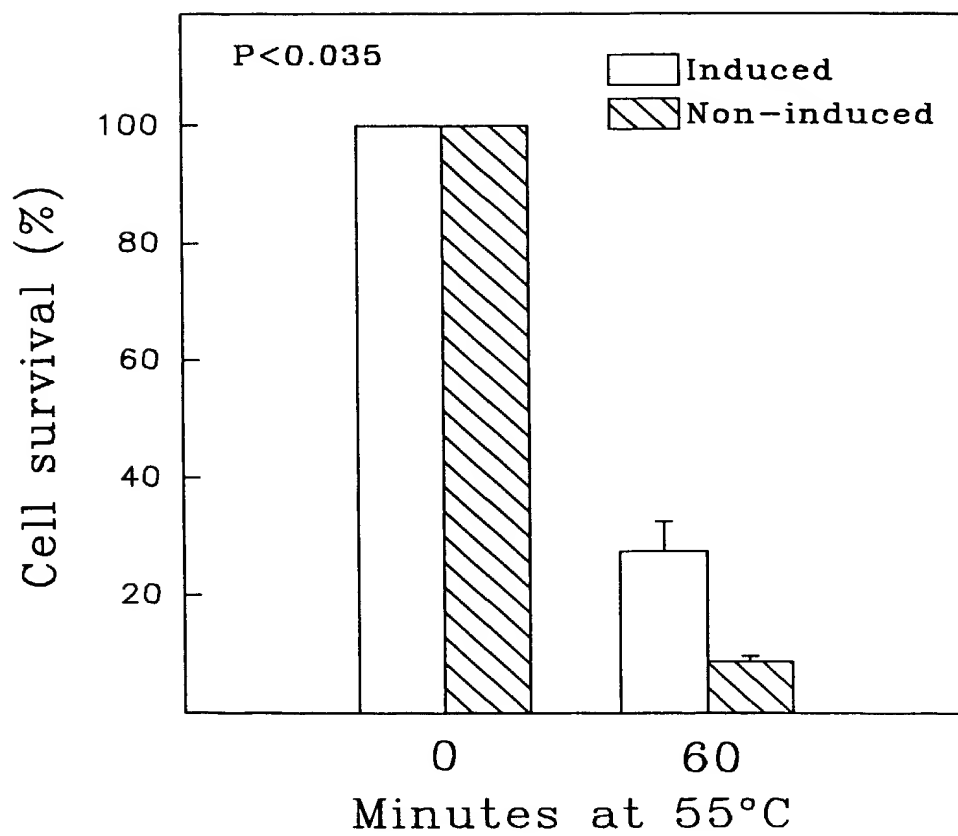
Fig. 2



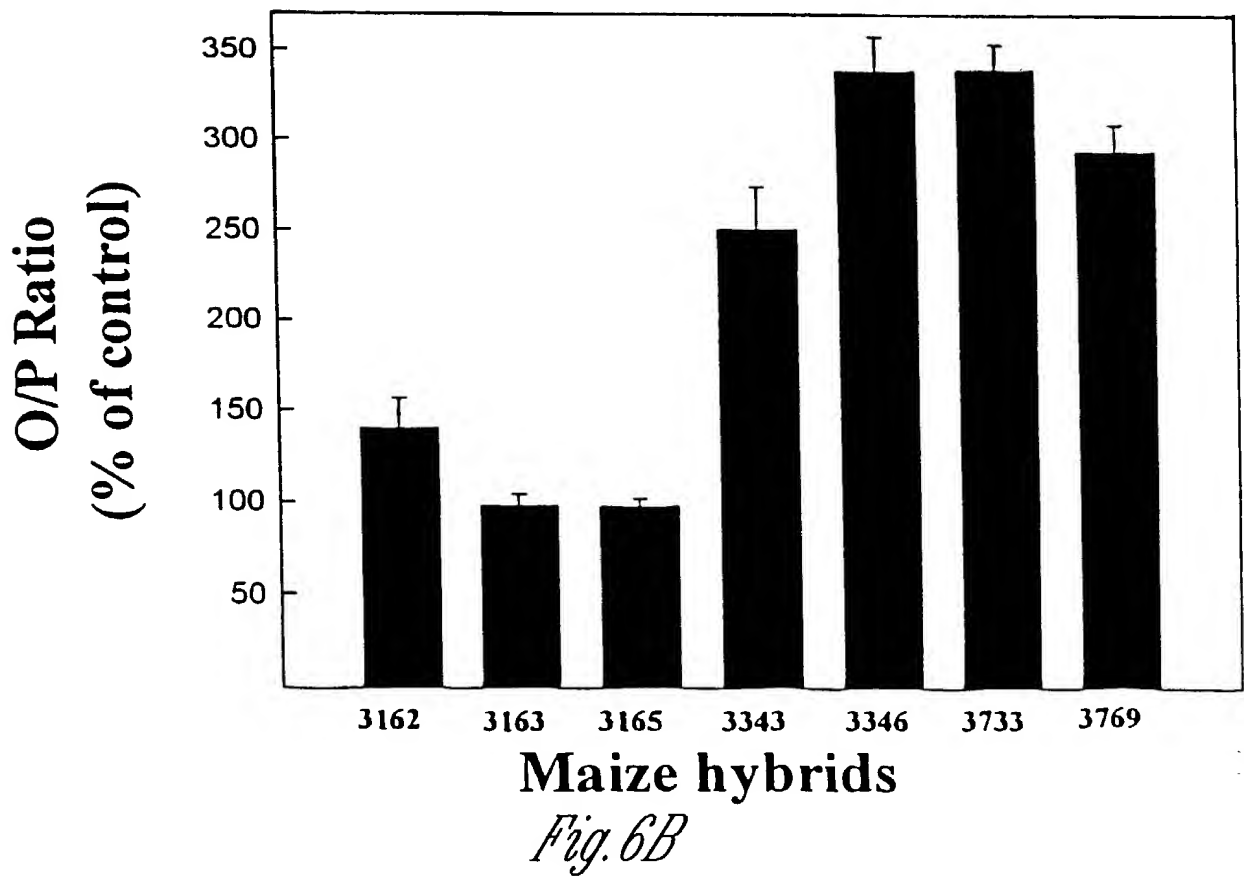
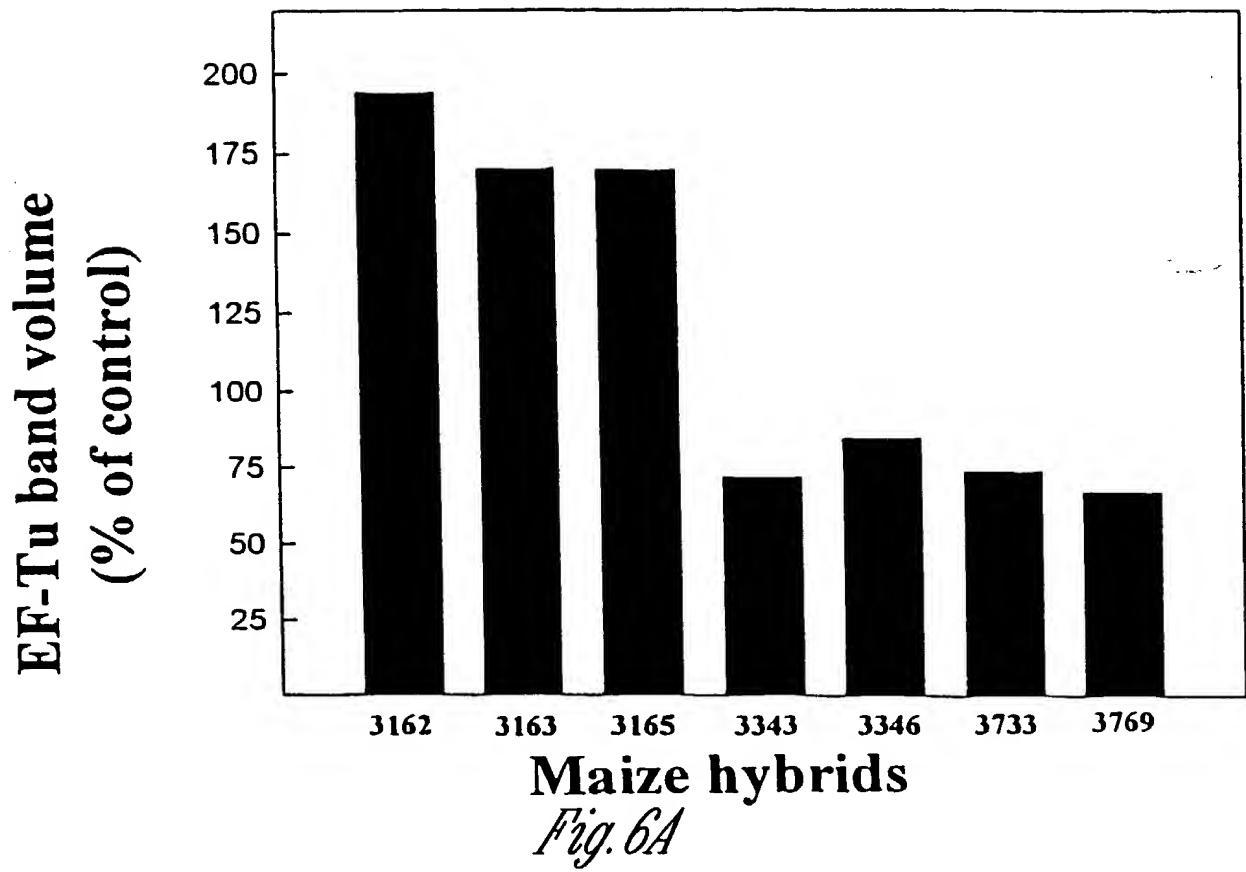
*Fig. 3*



*Fig. 4*



*Fig. 5*



SDS-PAGE gel analysis of EF-Tu protein levels. The gel shows three pairs of lanes labeled C (Control) and HS (Heat Shock) for three different heat-tolerant hybrids: 3162, 3163, and 3165. An arrow on the left points to the EF-Tu protein band. The protein levels are visibly higher in the HS lanes compared to the C lanes for all three hybrids.

Hybrid	Strain	EF-Tu Level (approximate)
3162	C	Low
	HS	High
3163	C	Low
	HS	High
3165	C	Low
	HS	High

(More heat-tolerant hybrids)

Western blot analysis showing EF-Tu protein levels in various hybrid strains. The blot displays four pairs of bands, each pair representing a different strain. The strains are labeled below the bands: 3343, 3346, 3733, and 3769. The label "(Less heat-tolerant hybrids)" is centered below the first two pairs of bands. An arrow on the left points to the first pair of bands, and the label "EF-Tu" is on the right, indicating the protein being detected.

*Fig. 6C*

AT TCCCAAATAA TCCCCACCTC CCGCTGCTGC  
 TCCGCCGCCC GCCATGGCCT CCCTCACCTC GGCGTCCACT TCACTCCTCT  
 TCCCGCAGGC CTCCTCATCC AGGAGCCGCA TCCGTCTCTC CACCCCCCTG  
 GGCTTCTCCG CGCAGCCTGC GCGGCTGCGG AGCCAGGGG GCGGCAGTGG  
 GCGCGCGGCG GCGCGGGCGC CTGCTGGTGG TGCGCGCGGC GAGGGGCAAG  
 TTCGAGCGCA CCAAACCACA CGTCAACATA GGCACCATCG GCCATGTGCA  
 CCACGGAAAG ACCACTCTCA CCGCCGCGCT CACCATGGTG CTCGCCTCCG  
 TCGGTGGCAG CGCGCCTAAG AAGTACGACG AGATCGACGC CGCCCCCGAG  
 GAGCGCGCCC GCGGTATCAC CATCAACACC GCCACCGTCG AGTACGAGAC  
 CGAGACCCGC CACTACGCAC ACGTCGACTG CCCC GGCCAC GCCGACTATG  
 TCAAGAATAT GATCACCGGC GCTGCGCAGA TGGACGGTGC CATCCTCGTC  
 GTATCCGGTG CCGACGGGCC CATGCCGCAG ACCAAAGAGC ACATCCTCCT  
 CGCCAAGCAA GTCGGTGTTT CCAAGATCGT TGTCTTCCTC AACAAAGAGG  
 ACATGGTTCG CGACGAGGAG CTGCTCGAGC TCGTCGAGCT CGAGGTCCGC  
 GAGCTGCTCA GCAACTACGA GTACGACGGC GACGACGTAC CAATCGTCGC  
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 AGCGCGGCGA CGATGAGTGG GTCGACTACA TCTTCTCGTT GGTTGATAAA  
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 CACAGTTCTA CATGCGGACA ACTGATGTG ACAGGGAGTG TGA CTACGAT  
 TATGAATGAC AAGGATGAGG AGGCGAAGAT GTGCATGCCT GGTGACCGTA  
 TCAAAATGAT TGTT CAGCTC ATCCAGCCTG TTGCTTGTGA GCAGGGTATG  
 AGGTTTGCTA TCCGTGAGGG TGTAAGACC GTTGGTGCCG GTGTCATCAA  
 CAAAATCATT GAGTAACTG GATATAACAT ATCCACCATG AGAATTTTCC  
 TTGTTTACTC AAAGCGACAT GCTCCGTAGT TGTTATTATG TGGTGAGTTT  
 TAGGGGTTGC TCATGTGCAA TTGTAGTATG ACACTTTTTT TTTGTCAAGT  
 GAATTTGCAT AATTTATGAC ATTCACGACA AAGATTCACA TATCTGGTTG  
 CAACTCATTT GGCTAAGAGG TGCCATCTAC TGTTAAAAA AAAAAAAAAA A

*Fig. 7*